

## Claims

- [c1] 1. A method for early identification of germline transformed plants comprising the steps of:
- (a) transforming meristematic or cotyledonary tissue with a plant expressible construct comprising at least one nucleic acid sequence encoding a protein to obtain transformed plant tissue;
  - (b) producing a shoot from the transformed plant tissue;
  - (c) growing roots from the shoot;
  - (d) assaying the roots for the presence of the nucleic acid sequence; and
  - (e) identifying roots that assay positive for said at least one nucleic acid sequence as putative germline transformed plants.
- [c2] 2. The method of claim 1 wherein said plant expressible construct comprises a first nucleic acid sequence encoding a protein conferring a trait to said plant, said trait selected from the group consisting of genes that encode for insect tolerance, pest tolerance, herbicide resistance, quality enhancement, yield enhancement, stress tolerance, and environmental tolerance.
- [c3] 3. The method of claim 1 wherein said plant expressible construct comprises at least two nucleic acid sequences each encoding a protein.
- [c4] 4. The method of claim 3 wherein a first nucleic acid sequence encodes a protein conferring a trait to said plant and the second nucleic acid sequence encodes a protein permitting transformed plants to be selected in the presence of a corresponding selection agent.
- [c5] 5. The method of claim 4 wherein the roots are grown in the presence of a selection agent that corresponds to the protein.
- [c6] 6. The method of claim 5 wherein the selection agent is kanamycin.
- [c7] 7. The method of claim 5 wherein the selection agent is glyphosate.
- [c8] 8. The method of claim 1 wherein the transformation is via *Agrobacterium* – mediated or particle–mediated methods.



